

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2002, 21:34:49 ; Search time 1445.89 Seconds
(without alignments)
15540.019 Million cell updates/sec

Title: US-09-635-521A-1
Perfect score: 1362
Sequence: 1 atggcttaccacagctctcc.....ttcagagacatgaatttga 1362

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues
TC: number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_on:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vl:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rnd:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rnd:*
36: em_htg_other:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1362	100.0	1362	9 AF034633	AF034633 Homo sapi
2	857	62.9	174494	2 AC068744	AC068744 Homo sapi
3	508.6	37.3	129676	9 AC079773	AC079773 Homo sapi
4	497.6	36.5	1890	6 AX136281	AX136281 Sequence
5	285	20.9	1797	10 AB041649	AB041649 Mus muscu
6	236.6	17.4	587	6 AX136698	AX136698 Sequence
7	165.2	12.1	1254	22 E11480	E11480 cDNA encod
8	164.8	12.1	4131	9 HSNEDURA	X70070 H.sapiens m
9	158.6	11.6	444	6 AX150120	AX150120 Sequence
10	150.4	11.0	110000	2 AL357872	AL357872 Homo sapi
11	150.4	11.0	114642	9 AL357033	AL357033 Human DNA
12	133.8	9.8	3917	10 AB017027	AB017027 Mus muscu
13	124.8	9.2	1239	9 AK026195	AK026195 Homo sapi
14	123.2	9.0	170695	2 AL391318	AL391318 Homo sapi
15	123.2	9.0	189476	2 AL157394	AL157394 Homo sapi
16	97.6	7.2	1569	5 HSNTR2REC	Y10148 H.sapiens m
17	96.2	7.1	1676	5 AF082210	AF082210 Spheroicoid
18	95.8	7.0	1342	6 E29334	E29334 Novel human
19	89.4	6.6	729	6 AX139107	AX139107 Sequence
20	89.4	6.6	801	6 AX147772	AX147772 Sequence
21	89.4	6.6	1239	9 AF242874	AF242874 Homo sapi
22	89.4	6.6	1248	9 AB041228	AB041228 Homo sapi
23	89.4	6.6	1248	9 AF292402	AF292402 Homo sapi
24	89.4	6.6	1298	9 AF272363	AF272363 Homo sapi
25	89.4	6.6	1594	6 AX109242	AX109242 Sequence
26	89.4	6.6	1594	6 AX109244	AX109244 Sequence
27	89.4	6.6	1658	6 AX109234	AX109234 Sequence
28	89.4	6.6	1658	6 AX109236	AX109236 Sequence
29	89.4	6.6	1658	6 AX109238	AX109238 Sequence
30	89.4	6.6	1658	6 AX109240	AX109240 Sequence
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34	83.6	6.1	6787	9 AF369786	AF369786 Homo sapi
35	83.6	6.1	145593	9 AC069523	AC069523 Homo sapi
36	82	6.0	870	9 HS060181	U60181 Human growt
37	82	6.0	1088	6 AX154584	AX154584 Sequence
38	82	6.0	1101	6 AX156354	AX156354 Sequence
39	82	6.0	1101	6 HS060179	U60179 Human growt
40	82	6.0	1122	6 AR156354	AR156354 Sequence
41	80.4	5.9	145272	2 AC016938	AC016938 Homo sapi
42	78.6	5.8	836	6 AR156355	AR156355 Sequence
43	77.2	5.7	1092	6 AR156357	AR156357 Sequence
44	77.2	5.7	1350	6 AB001982	AB001982 Rattus no
45	77.2	5.7	3129	6 AR156356	AR156356 Sequence

ALIGNMENTS

RESULT 1
AF034633 LOCUS
DEFINITION Homo sapiens orphan G protein-coupled receptor (GPR39) mRNA,
complete cds.
ACCESSION AF034633
VERSION AF034633.1 GI:2654160
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1362)
McKee,K.K., Tan,C.P., Palyha,O.C., Liu,J., Feiginger,S.D.,
Hreniuk,D.L., Smith,R.G., Howard,A.D. and Van der Ploeg,U.H.
Cloning and characterization of two human G protein-coupled
receptor genes (GPR38 and GPR39) related to the growth hormone
secretagogue and neurotensin receptors
JOURNAL Genomics 46 (3), 426-434 (1997)
MEDLINE 9810578

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 174494)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 2, clone RP11-666P13
Unpublished
2 (bases 1 to 174494)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavsky,L., Bouknight,B., Brown,A., Burkett,G., Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Deatello,K., Dewar,K., Diaz,J.S., Dodge,S., Domingo,M., Doyle,M., Ferreira,P., Fitzhugh,N., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hages,B., Heatford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lechoczy,J., Levine,R., Liu,C., Liu,G., Locke,K., MacDonald,P., Margulis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R., Meldrum,J., Menus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N., Pisanì,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testave,S., Theodore,J., Tirrell,A., Travers,M., Triggilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Submitted (08-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.
On Oct 4, 2000 this sequence version replaced gi:7717151.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/MIT Center for Genome Research
Genome Center
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L9278
Center clone name: 666_P-13

----- Summary Statistics
Sequencing vector: M13: M77815: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 163890 bases at least Q40
Consensus quality: 169058 bases at least Q30
Consensus quality: 171182 bases at least Q20
Insert size: 170000: agarose-fp
Insert size: 172394: sum-of-ctrls
Quality coverage: 4.9 in Q20 bases; sum-of-ctrls
Quality coverage: 4.8 in Q20 bases; sum-of-ctrls

* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 17735: contig of 17735 bp in length
* 17736 17835: gap of 100 bp
* 17836 45012: contig of 27177 bp in length
* 45013 45112: gap of 100 bp
* 45113 46230: contig of 1118 bp in length
* 46231 46330: gap of 100 bp
* 46331 47605: contig of 1275 bp in length
* 47606 47705: gap of 100 bp
* 47706 49342: contig of 1637 bp in length
* 49343 49442: gap of 100 bp
* 49443 51470: contig of 2028 bp in length
* 51471 51570: gap of 100 bp

FEATURES

SOURCE

51571 53723: contig of 2153 bp in length
* 53724 53823: gap of 100 bp
* 53824 56799: contig of 2976 bp in length
* 56800 56899: gap of 100 bp
* 56900 60103: contig of 3204 bp in length
* 60104 60203: gap of 100 bp
* 60204 64890: contig of 4687 bp in length
* 64891 64990: gap of 100 bp
* 64991 70638: contig of 5648 bp in length
* 70639 70738: gap of 100 bp
* 70739 76977: contig of 6239 bp in length
* 76978 77077: gap of 100 bp
* 77078 82744: contig of 5667 bp in length
* 82745 82844: gap of 100 bp
* 82845 90681: contig of 7837 bp in length
* 90682 90781: gap of 100 bp
* 90782 98252: contig of 7471 bp in length
* 98253 98352: gap of 100 bp
* 98353 107826: contig of 9474 bp in length
* 107827 107926: gap of 100 bp
* 107927 117679: contig of 9753 bp in length
* 117680 117779: gap of 100 bp
* 117780 129303: contig of 11524 bp in length
* 129304 129403: gap of 100 bp
* 129404 140999: contig of 11596 bp in length
* 141000 141099: gap of 100 bp
* 141100 151374: contig of 10275 bp in length
* 151375 151474: gap of 100 bp
* 151475 174223: contig of 22749 bp in length
* 174224 174323: gap of 100 bp
* 174324 174494: contig of 171 bp in length.

Location/Qualifiers
1. 174494
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone.lib="RP11-666P13"
/clone.lib="RP11-11 Human Male BAC"
1. 17735
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vector_side:left
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/note="assembly-fragment"
45113..46230
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46331..47605
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Db	119732	TGTAACAGGtGTCTCTCCACAGTTTGGGGGGGtTTCGTGCAGAGtCTGTGTGCCGCC	119791
QY	1088	tgctgcctgcagcaacgccaacaacagagaagcgctcgcgtacatgacatccacaacg	1147
Db	119792	TGTGCGTGCAGCAACGCCAACACACAGAGAAGGCGCTGCCGCTACATGCGCACTCCACACCG	119851
QY	1148	acagcgccgccttctgtgcagcgcccgltgtctcttcgcgtcccgcgcgcaagtcctctgcaa	1207
Db	119852	ACAGCGCCGCTTGTGTGCACGCGCCGCTGTGCTTCGTGGCGTCCGGCGCCAACTTCCTGCAA	119911
QY	1208	ggagaaactgtgagaagaatttctttaaagcatttcaagcagcgccgagcccgacttaagt	1267
Db	119912	GGGAAACTGAGAAATTTTCTTAAGCACTTTTCAGAGCGAGCGCCGAGCCCAAGCTCAAGT	119971
QY	1268	ccgaagtattgagttctcgatctcaatctgagcgccaactaagcgcgaaacagccaattctg	1327
Db	119972	CCCAAGTATTGAGTCTCGAATCTCAATAGGCCCAACTCAGGCGGAAACCGCAACTTCTG	120031
QY	1328	ctgcagaagaatgttttccagaagaatgaatttga	1362
Db	120032	CTGCAGAGAAATGCTTTTCAGAGCATCAAAATTGGA	120066

RESULT	4	-
AXI36281/c		
LOCUS	AXI36281	1890 bp DNA PAT 30-MAY-2001
DEFINITION	Sequence 203 from Patent EP1067182.	
ACCESSION	AXI36281	
VERSION	AXI36281.1	GI:14272687
KEYWORDS		
SOURCE	human.	

REFERENCE AUTHORS	TITLE JOURNAL	FEATURES
1 (bases 1 to 1890) Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.	Secretory protein or membrane protein Patent: EP 1067182-A 203 10-JAN-2001; Helix Research Institute (JP)	
	Location/Qualifiers	

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/organism="Homo sapiens"
/db_xref="taxon:9606"
274. .771
CDS

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Query Match	36.5%	Score 497.6;	DB 6;	Length 1890;
Best Local Similarity	99.0%;	Pred. No. 1.5e-89;		
Matches 511; Conservative	0;	Mismatches 4;	Indels 1;	Gaps 1.

QY	848	tctctcttgagcctgcatgtgttgcgaattgacgcatatgctgagtcgccaacagattgga	907
Db	1651	TCGCCCCAGGCGCTGATTTGTTGACATTBTGGCCGTATGCTGGATGCCCAACCAACGATTTCCGA	1599
QY	908	ggaatcatggtctgcygcaccaaccgaacgacttgcagcaggtcctactctcggcggtaca	967
Db	1591	GGATTCATGTGCTGGCGGCAACCAACGACGACTGGACGAGGTCTCTACTTCGCGGGGTACA	1532
QY	968	tgatctctctccctctctgcgagacgtttttctactcaagctcgggtcatcaacccgcttc	1027

Db	1531	TGATCCCTCCCTCCCTCTCTCGGAACGCTTTTCTACTCAGCTGCGATCGATCAACCCGGCTCC	1472
QY	1028	tgtaacacggtgtcctctcgcaagcaatttcgcgcgagtgctctgtgcagagtgctgtgcgcgc	1087
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QY	1088	tgctgctgcacgaacgcgcacacgaagaagcgctctgagtgatcatgacgtccaccacgcg	1147
Db	1411	TGTCGCTGCAGACGCGCCAAACCAAGAAAGCGCTGCGCTACATGCGCACTTCACACACG	1355
QY	1148	acagcgcgcctctgtgcgaacgcgcgctgtcctctgcgtccgcgcgcgcgcgcctctgcga	1207
Db	1351	ACAGACGCGCGCTTGTGTGCAGCGCCCGCTGTCTTCGCGTCCCGGCGCAGTCTCTGCAA	1292
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Db	1291	GGGGAACCTGAGAAGATTCTTAAAGCACTTTTCAAGCGGAGGCGGAGGCCCAAGTCFAG	1233
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Db	1231	TCCCAAGTCATTGATGCTCTCGATCTACTATGAGCCCAATCAGGCGCGCAAAACACGCAATCT	1172
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LOCUS	Mus musculus brain cDNA, clone MNcB-0671.			
DEFINITION	AB041649			
ACCESSION	AB041649.1 GI:7670499			
VERSION	fis (full insert sequence).			
KEYWORDS	Mus musculus (strain:C57BL) adult female cDNA to mRNA,			
SOURCE				

ORGANISM Mus musculus

REFERENCE
AUTHORS
Osada, N., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Sugano, S. and
1 (sites)
Bukayeva; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

TITLE	isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method
JOURNAL	unpublished (2000)
REFERENCE	2 (bases 1 to 1797)
AUTHORS	Hashimoto, K., Osada, N., Kusuda, J. and Sugano, S.
TITLE	Direct Submission
JOURNAL	Submitted (13-Apr-2000) to the DDBJ/EMBL/Genbank databases.

Division of Genetic Resources, 23-1, Toyama 1-chome, Shinjuku-ku
Tokyo 162-8640, Japan (E-mail: khashi@nih.go.jp,
URL: <http://www.nih.go.jp/yoken/genebank/>,
Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181)
URL: <http://www.nih.go.jp/yoken/genebank/>

Vector: pME185-FLJ3
1st strand cDNA was primed with an oligo(dT) primer
[ATGTGGCCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with SfiI and size selection was performed to
exclude fragments <1.5kb. The SfiI-digested PCR product was cloned
into distinct DraIII sites of pME185-FLJ3. XhoI sites just outside
the DraIII sites can be used to isolate the cDNA insert. Library
was constructed by Sugano et al. (University of Tokyo, Institute of
Medical Science). Custom primer used for sequencing (5' end primer
[CTTCTCCTCTTAAGAAGTCGG]; 3' end primer
[CGACCTGCAGCTCGAGCACAA]).
A part of this sequence is reported in AU053640.
Location/Qualifiers
1..1797
/organism="Mus musculus"
source

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325..750
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NCTVAVDDMCQKEVTEDSASIMTKSCASSAACIIASAGYOSFCSPKIMSVCSICNN
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BASE COUNT      391 a      487 c      511 g      408 t
ORIGIN

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DB 1716	GACTGATGTGTGTGACCTTGTGGCCGTGTGTGATGGCCAAATCGAATCGACGATCATG	1657		
QY 917	ctgcggcccaaacccaagaacagcagtcggagaggtcccaattcccgagctacatgatccctc	976		
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QY 977	tcacctctcggagacglttttcttaactcagctcgtatgcatcaaccgcctctgttacaag	1036		
DB 1596	TGCCCTCTCTGTATACCTCTTCTTACCTCAGCTCTGTGTCAACCCCTCTCTTACAAAG	1537		
QY 1037	tgctctcgacacagtttcggagggtgtctgtcaaggtgctgtctccgcctgtcgtc	1096		
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QY 1097	agccagcccaacacagagaaagcgcctcgcgctacatcgcacatccacacacagacgcgcc	1156		
DB 1476	AGCATGCCAACCAACAGAAAGGCCAGGCTGCCCGCTTCATCTCCACCAAGACAGACCA	1417		
QY 1157	gcttctgtcagcgcacctgtctctcgcctc-----cggcgcagatcctctgcgaaga	1210		
DB 1416	GCTCAGCCCGCAGCCCCCTCATCTTCTCTTAAGCTCCGCCGACAGTAACCTTCTTCCAGGA	1357		
QY 1211	gaacgcgagaagaatttctttaaagcatttcaagagcagagccgaagc---ccagtlcaagt	1267		
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DB 1236	CCCCAGAAATAGTTTACGAGGACGAGGAATATGA	1202		
RESULT 6				
AX136698	587 bp	DNA	PAT	30-MAY-2001
LOCUS	Sequence 620 from Patent EP1067182.			
DEFINITION	AX136698			
ACCESSION	AX136698.1			
VERSION	GI:14273102			
KEYWORDS	human.			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.			

TITLE	Secretory protein or membrane protein				
JOURNAL	Patent: EP 1067182-A 620 10-JAN-2001;				
FEATURES	Helix Research Institute (JP)				
SOURCE	Location/Qualifiers				
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	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
BASE COUNT	117 a	162 c	140 g	162 t	6 others
ORIGIN					

Query Match	17.4%	Score 236.6	DB 6	Length 587
Best Local Similarity	85.8%	Pred. No. 2.4e-37		
Matches 296	Conservative	0	Mismatches 43	Indels 6
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Db 240	TCCTGCCAGGGCTGATGTTGTGTGACANTGGCCGTATGCTGATGCCCCAACAGATTCCGGA	299		
QY 908	ggatcatgtcgtcgcggccaaacccaagcaagcagctctgacagcgggttccattccgcggggtaca	967		
Db 300	GGATCATGTGCTGCTGCGCCAAACCCAGAGCAGACTGGAGGAGGTCCTACTCCGGGCGCTACA	359		
QY 968	tgtacttcctccctcccttctcgagagacgcttttctcaactcagctcgtgcatcaaacccgtcc	1027		
Db 360	TGATCTCTCTCCCTCCCTCTCTCGAGACGTTTTTCTTACCTCAGCTGTGCTATCAACCCGCTTC	419		
QY 1028	tgtacacagctgtctctcgcagcagttctgcgcgggtlgtctgtcagtgctgtcgtcgcgc	1087		
Db 420	TGTACACAGTGTTCTCCCTCGAACANTTCGGCGGGGtGtCGTCAGNTGTC--TGGCTTCCGCC	477		
QY 1088	tgtcgtcgcagcagcgcacacacagcagagaagcgtctgcgcgtacatgtgacatccacacacg	1147		
Db 478	TGTCTGCTTGAACACGCCAACCCACGAGAGCGCTGNGCG-ACATGGCGACTCACAAAC--	534		
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RESULT 7				
ID E11480	standard; RNA; HUM; 1254 BP.			
XX AC E11480;				
XX SV E11480.1				
XX DT 08-OCT-1997 (Rel. 52, Created)				
XX DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)				
XX DE CDNA encoding human neurotensin receptor protein.				
XX JP 1996143597-A/1.				
OS Homo sapiens (human)				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;				
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
XX [1]				
RN 1-1254				
RP Onda H., Oogi K., Hinuma K., Masuo Y.;				
RA "HUMAN NEUROTENSIN RECEPTOR PROTEIN, ITS PRODUCTION AND USE";				
RT Patent number JP1996143597-A/1. 04-JUN-1996.				
RL TAKEDA CHEM IND LTD.				
XX OS Homo sapiens (human)				
CC PN JP 1996143597-A/1				
CC PD 04-JUN-1996				
CC PF 24-NOV-1994 JP 1994289882				
CC PI ONDA HARUO, OOGI KAZUHIRO, HINUMA KUNIJU, MASUO YOSHINORI				
CC PC OKI4772,A61K38/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,				
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VERSION AL357872.15 GI:11414584
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 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 367980)
 AUTHORS Plumb, B.
 TITLE Direct Submission
 JOURNAL Submitted (08-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 On Nov 28, 2000 this sequence version replaced gi:11340280.
 COMMENT
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk
 ----- Project Information
 Center project name: ba308p
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: piasm4; version 1.08752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 346090 bases at least Q40
 Consensus quality: 353078 bases at least Q30
 Consensus quality: 356859 bases at least Q20
 Insert size: 362580; sum-of-contigs
 Insert size: 177412; 7.0% error; agarose-fp
 Quality coverage: 4.17x in Q20 bases; sum-of-contigs Quality
 coverage: 9.44x in Q20 bases; agarose-fp

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 55 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 3371: contig of 3371 bp in length
 * 3372 3471: gap of 100 bp
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 * 6279 6378: gap of 100 bp
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 * 59224 59323: gap of 100 bp
 * 59324 63598: contig of 4275 bp in length
 * 63599 63698: gap of 100 bp
 * 63699 77580: contig of 13882 bp in length
 * 77581 77680: gap of 100 bp
 * 77681 81030: contig of 3350 bp in length
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